Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (previously presented): A method for separating a nucleic acid containing both a first nucleotide sequence type and a second nucleotide sequence type from a sample also comprising nucleic acids not containing both the first nucleotide sequence type and the second nucleotide sequence type, said method comprising:

(a) coupling a first hybridization probe configured for hybridizing to the first nucleotide sequence type to a magnetically responsive first bead via a first pair of complexing agents to form a first probe-bead complex, and coupling a second hybridization probe configured for hybridizing to the second nucleotide sequence type to a magnetically non-responsive second bead, which is distinguishable from the first bead by size, charge, color, or attachability to a solid support, via a second pair of complexing agents to form a second probe-bead complex;

(b) mixing the first probe-bead complex and the second probe-bead complex with the sample to form a mixture under conditions such that the first hybridization probe hybridizes to the first nucleotide sequence type and the second hybridization probe hybridizes to the second nucleotide sequence type;

(c) separating the first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof from the ~~first~~ mixture by applying magnetic force to the mixture and then washing the isolated first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof, thereby obtaining a fraction comprising the first nucleotide sequence type;

(d) separating the second probe-bead complex and nucleic acids hybridized to the second hybridization probe portion thereof from the fraction comprising the first nucleotide sequence type according to the properties of the distinguishable feature of the second bead and then washing to remove nucleic acids not hybridized to the second hybridization probe, thereby separating the nucleic acid containing both the first nucleotide sequence type and the second

nucleotide sequence type from nucleic acids not containing both the first nucleotide sequence type and the second nucleotide sequence type.

Claim 2 (previously presented): A method for separating and quantifying a nucleic acid containing both a first nucleotide sequence type and a second nucleotide sequence type from a sample also comprising nucleic acids not containing both the first nucleotide sequence type and the second nucleotide sequence type comprising:

(a) coupling a first hybridization probe configured for hybridizing to the first nucleotide sequence type to a magnetically responsive first bead via a first pair of complexing agents to form a first probe-bead complex, and coupling a second hybridization probe configured for hybridizing to the second nucleotide sequence type to a magnetically non-responsive second bead, which comprises a feature distinguishable from the first bead by size, charge, color, or attachability to a solid support, via a second pair of complexing agents to form a second probe-bead complex;

(b) mixing the first probe-bead complex and the second probe-bead complex with the sample to form a mixture under conditions such that the first hybridization probe hybridizes to the first nucleotide sequence type and the second hybridization probe hybridizes to the second nucleotide sequence type;

(c) separating the first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof from the mixture by applying magnetic force to the mixture for isolating the first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof and then washing the isolated first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof, thereby obtaining a fraction comprising the first nucleotide sequence type;

(d) separating the second probe-bead complex and nucleic acids hybridized to the second hybridization probe portion thereof from the fraction comprising the first nucleotide sequence type according to the properties of the distinguishable feature of the second bead and then washing to remove nucleic acids not hybridized to the second hybridization probe, thereby separating the nucleic acid containing both the first nucleotide sequence type and the second

nucleotide sequence type from nucleic acids not containing both the first nucleotide sequence type and the second nucleotide sequence type; and

(e) determining the amount of nucleic acid containing both the first nucleotide sequence type and the second nucleotide sequence type as a proportion of total nucleic acids present in the sample.

Claim 3 (currently amended): A method for diagnosing a disease or disorder associated with the presence in an individual of a nucleic acid comprising a first nucleotide sequence type and a second nucleotide sequence type comprising:

(a) coupling a first hybridization probe configured for hybridizing to the first nucleotide sequence type to a magnetically responsive first bead via a first pair of complexing agents to form a first probe-bead complex, and coupling a second hybridization probe configured for hybridizing to the second nucleotide sequence type to a magnetically non-responsive second bead via a second pair of complexing agents to form a second probe-bead complex;

(b) obtaining a nucleic acid sample from an individual to be tested and mixing the first probe-bead complex and the second probe-bead complex with the sample to form a mixture under conditions such that the first hybridization probe hybridizes to the first nucleotide sequence type and the second hybridization probe hybridizes to the second nucleotide sequence type;

(c) separating the first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof from the ~~first~~ mixture by applying magnetic force to the ~~first~~ mixture for isolating the first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof and then washing the isolated first probe-bead complex and nucleic acids hybridized to the first hybridization probe portion thereof, thereby obtaining a fraction comprising the first nucleotide sequence type; and

(d) separating the second probe-bead complex and nucleic acids hybridized to the second hybridization probe portion thereof from the fraction comprising the first nucleotide sequence type according to the properties of the distinguishable feature of the second bead and then washing to remove nucleic acids not hybridized to the second hybridization probe, thereby separating the nucleic acid containing both the first nucleotide sequence type and the second

nucleotide sequence type from nucleic acids not containing both the first nucleotide sequence type and the second nucleotide sequence type;

(e) detecting the presence of the nucleic acid containing both the first nucleotide sequence type and the second nucleotide sequence type; and

(f) quantifying the nucleic acid containing both the first nucleotide sequence type and the second nucleotide sequence type, wherein the presence or increased presence of the nucleic acid containing ~~contanining~~ both the first nucleotide sequence type and the second nucleotide sequence type supports a diagnosis of the presence of the disease or disorder, and wherein the absence or decreased presence of a nucleic acid containing both the first nucleotide sequence type and the second nucleotide sequence type supports a diagnosis of the absence of the disease or disorder.

Claim 4 (cancelled)

Claim 5 (previously presented): A process for separating objects bearing at least a first binding site and a second binding site from other objects that do not bear both said first binding site and said second binding site, comprising

(a) mixing a first binder/bead composition, comprising a magnetically responsive bead coupled to a first binder that binds the first binding site on said objects, and a second binder/bead composition, comprising a magnetically non-responsive bead coupled to a second binder that binds the second binding site on said objects, wherein said magnetically non-responsive bead comprises a feature distinguishable from the first bead by size, charge, color, or attachability to a solid support, with a fluid containing said objects and said other objects to form a mixture such that said first binder binds said first binding site to form a first complex and said second binder binds said second binding site to form a second complex;

(b) contacting said mixture with a magnetic field such that said first complex is attracted to said magnetic field and removing said first complex from said mixture to form a fraction; and

(c) separating said objects from said fraction comprising said other objects by the size, charge, color, or attachability to a solid support that distinguishes the magnetically non-responsive bead from the magnetically responsive bead.

Claim 6 (previously presented): The process of claim 5 wherein said objects are selected from the group consisting of nucleic acids, proteins, chromosomes, cells, and organelles.

Claims 7-26 (cancelled)